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count
mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, and expectation (E) of 10, a cutoff of 100, M=5, N=-4, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff & Henikoff (1989) Proc. Natl. Acad. Sci. USA 89:10915).--

IN THE CLAIMS:

Please cancel claim 21 without prejudice or disclaimer, the subject matter thereof having been incorporated into independent claim 2.

Please amend claims 1-4, 6-11, 13, 15 and 16 as follows:

1. (Five Times Amended) An isolated rpoB nucleic acid molecule consisting of at least about 100 contiguous bases of a sequence selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6, 8, 9 and 10.

2. (Five Times Amended) An isolated nucleic acid molecule consisting of a rpoB sequence selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6, 7, 8, 9 and 10.

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3. (Five Times Amended) A probe which is the complement of a rpoB sequence selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6, 7, 8, 9, and 10.

4. (Four Times Amended) A method of classifying a mycobacteria, comprising providing a sample comprising a mycobacterial rpoB target nucleic acid from a mycobacteria;

determining the sequence of a segment of at least 50 contiguous bases from the target nucleic acid;

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comparing the determined sequence to at least one sequence selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6, 7, 8, 9, and 10; and
classifying the mycobacteria from the extent of similarity of the compared sequences.

6. (Four Times Amended) The method of claim 4, wherein the determined sequence is compared with at least nine sequences selected from the group consisting SEQ ID NOS: 2, 3, 4, 5, 6, 7, 8, 9, and 10.

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7. (Four Times Amended) A method of classifying a mycobacteria, comprising providing a sample comprising a mycobacterial rpoB target nucleic acid; determining the identity of one or more bases in the target sequence at one or more positions corresponding to one or more bases in a sequence selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6, 7, 8, 9, and 10, wherein the one or more bases of the sequence selected from the group consisting of SEQ ID NOS. 2, 3, 4, 5, 6, 7, 8, 9, and 10 differ from the corresponding one or more bases in SEQ ID NO. 1 when the sequences are maximally aligned, the identity of the one or more bases characterizing the species of mycobacteria that is present in the sample;

comparing the identified one or more bases in the target sequence to at least one sequence selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6, 7, 8, 9, and 10; and

classifying the mycobacteria from the extent of similarity between the one or more bases identified in the target sequence and the corresponding one or more bases in the compared sequences.

8. (Four Times Amended) The method of claim 7, wherein the identity of at least 10 bases in the target nucleic acid at positions corresponding to the one or more bases in the sequence selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6, 7, 8, 9, and 10 is determined.

9. (Five Times Amended) The method of claim 8, wherein the identity of at least 20 bases in the target sequence at positions corresponding to the one or more bases in the

sequence selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6, 7, 8, 9, and 10 is determined.

10. (Five Times Amended) The method of claim 9, further comprising comparing the at least 20 determined bases with at least 20 bases occupying corresponding positions in each of at least nine sequences selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6, 7, 8, 9, and 10.

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11. (Five Times amended) A polynucleotide probe or primer that hybridizes under stringent hybridization conditions to at least a contiguous segment of a mycobacterial *rpoB* sequence selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6, 8, 9, and 10 or its complement without hybridizing to the *M. tuberculosis* sequence of SEQ ID NO: 1 or its complement, wherein the contiguous segment of the mycobacterial *rpoB* sequence includes at least about 5 bases of the mycobacterial *rpoB* sequence selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6, 8, 9, and 10 which differ from the corresponding at least about 5 bases in SEQ ID NO: 1 when the sequences are maximally aligned; wherein said stringent hybridization conditions comprise 5 x SSPE and a temperature of 25-30°C.

12. (Three Times Amended) The polynucleotide of claim 11 that is a probe.

13. (Five Times Amended) The polynucleotide of claim 12, wherein a central position of the probe aligns with the one or more bases of a sequence selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6, 8, 9, and 10 which differ from the corresponding one or more bases in SEQ ID NO: 1 when the sequences are maximally aligned.

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15. (Five Times Amended) The polynucleotide of claim 14, wherein the 3' end of the primer aligns with the one or more bases of a sequence selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6, 8, 9, and 10 which differ from the corresponding one or more bases in SEQ ID NO: 1 when the sequences are maximally aligned.

16. (Four Times Amended) The polynucleotide of claim 11 that hybridizes under stringent hybridization conditions to at least 100 contiguous bases of a mycobacterial *rpoB* sequence selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6, 8, 9, and 10 or its
